

# Alexander Schmidt

## List of Publications by Year in descending order

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88  
papers

10,867  
citations

41344

49  
h-index

43889

91  
g-index

95  
all docs

95  
docs citations

95  
times ranked

15547  
citing authors

#	ARTICLE	IF	CITATIONS
1	The quantitative proteome of a human cell line. <i>Molecular Systems Biology</i> , 2011, 7, 549.	7.2	691
2	The quantitative and condition-dependent <i>Escherichia coli</i> proteome. <i>Nature Biotechnology</i> , 2016, 34, 104-110.	17.5	655
3	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. <i>Cell</i> , 2012, 151, 671-683.	28.9	513
4	A novel strategy for quantitative proteomics using isotope-coded protein labels. <i>Proteomics</i> , 2005, 5, 4-15.	2.2	477
5	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	12.6	440
6	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765.	27.8	402
7	Identification of cross-linked peptides from large sequence databases. <i>Nature Methods</i> , 2008, 5, 315-318.	19.0	379
8	A Mass Spectrometric-Derived Cell Surface Protein Atlas. <i>PLoS ONE</i> , 2015, 10, e0121314.	2.5	356
9	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	27.8	307
10	Large-Scale Quantitative Assessment of Different In-Solution Protein Digestion Protocols Reveals Superior Cleavage Efficiency of Tandem Lys-C/Trypsin Proteolysis over Trypsin Digestion. <i>Journal of Proteome Research</i> , 2012, 11, 5145-5156.	3.7	298
11	<b>SuperHirn</b> – a novel tool for high resolution LC-MS-based peptide/protein profiling. <i>Proteomics</i> , 2007, 7, 3470-3480.	2.2	295
12	Protein Identification False Discovery Rates for Very Large Proteomics Data Sets Generated by Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2405-2417.	3.8	282
13	Quantification of mRNA and protein and integration with protein turnover in a bacterium. <i>Molecular Systems Biology</i> , 2011, 7, 511.	7.2	267
14	Phenotypic Variation of <i>Salmonella</i> in Host Tissues Delays Eradication by Antimicrobial Chemotherapy. <i>Cell</i> , 2014, 158, 722-733.	28.9	259
15	Ubiquitin-related modifier Urm1 acts as a sulphur carrier in thiolation of eukaryotic transfer RNA. <i>Nature</i> , 2009, 458, 228-232.	27.8	245
16	ATM-Dependent and -Independent Dynamics of the Nuclear Phosphoproteome After DNA Damage. <i>Science Signaling</i> , 2010, 3, rs3.	3.6	245
17	The Plk1-dependent Phosphoproteome of the Early Mitotic Spindle. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.004457.	3.8	201
18	Critical assessment of proteome-wide label-free absolute abundance estimation strategies. <i>Proteomics</i> , 2013, 13, 2567-2578.	2.2	190

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19	PhosphoPepâ€”a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. <i>Molecular Systems Biology</i> , 2007, 3, 139.	7.2	168
20	Global 3' UTR shortening has a limited effect on protein abundance in proliferating T cells. <i>Nature Communications</i> , 2014, 5, 5465.	12.8	164
21	Parallel Exploitation of Diverse Host Nutrients Enhances Salmonella Virulence. <i>PLoS Pathogens</i> , 2013, 9, e1003301.	4.7	163
22	Bacterial persistence is an active $\sigma^S$ stress response to metabolic flux limitation. <i>Molecular Systems Biology</i> , 2016, 12, 882.	7.2	158
23	The Standard Protein Mix Database: A Diverse Data Set To Assist in the Production of Improved Peptide and Protein Identification Software Tools. <i>Journal of Proteome Research</i> , 2008, 7, 96-103.	3.7	156
24	Disparate Impact of Oxidative Host Defenses Determines the Fate of Salmonella during Systemic Infection in Mice. <i>Cell Host and Microbe</i> , 2014, 15, 72-83.	11.0	151
25	Protein synthesis rates and ribosome occupancies reveal determinants of translation elongation rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15023-15032.	7.1	150
26	Adenylation control by intra- or intermolecular active-site obstruction in Fic proteins. <i>Nature</i> , 2012, 482, 107-110.	27.8	149
27	Evaluation and Improvement of Quantification Accuracy in Isobaric Mass Tag-Based Protein Quantification Experiments. <i>Journal of Proteome Research</i> , 2016, 15, 2537-2547.	3.7	148
28	Visual proteomics of the human pathogen <i>Leptospira interrogans</i> . <i>Nature Methods</i> , 2009, 6, 817-823.	19.0	142
29	Hepatic stellate cells suppress NK cell-sustained breast cancer dormancy. <i>Nature</i> , 2021, 594, 566-571.	27.8	139
30	Quantitative interaction proteomics using mass spectrometry. <i>Nature Methods</i> , 2009, 6, 203-205.	19.0	136
31	An Integrated, Directed Mass Spectrometric Approach for In-depth Characterization of Complex Peptide Mixtures. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2138-2150.	3.8	127
32	Estimation of Absolute Protein Quantities of Unlabeled Samples by Selected Reaction Monitoring Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013987.	3.8	117
33	S6K1-Mediated Disassembly of Mitochondrial UPR/PP1 <sup>3</sup> Complexes Activates a Negative Feedback Program that Counters S6K1 Survival Signaling. <i>Molecular Cell</i> , 2007, 28, 28-40.	9.7	101
34	Polycomb purification by in vivo biotinylation tagging reveals cohesin and Trithorax group proteins as interaction partners. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5572-5577.	7.1	92
35	Absolute quantification of microbial proteomes at different states by directed mass spectrometry. <i>Molecular Systems Biology</i> , 2011, 7, 510.	7.2	91
36	Directed mass spectrometry: towards hypothesis-driven proteomics. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 510-517.	6.1	90

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37	Analysis of Cell Surface Proteome Changes via Label-free, Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 624-638.	3.8	84
38	The Gcn4 transcription factor reduces protein synthesis capacity and extends yeast lifespan. <i>Nature Communications</i> , 2017, 8, 457.	12.8	83
39	Systematic Proteomic Analysis Identifies $\beta$ -Site Amyloid Precursor Protein Cleaving Enzyme 2 and 1 (BACE2 and BACE1) Substrates in Pancreatic $\beta$ -Cells. <i>Journal of Biological Chemistry</i> , 2013, 288, 10536-10547.	3.4	82
40	From coarse to fine: the absolute <i>Escherichia coli</i> proteome under diverse growth conditions. <i>Molecular Systems Biology</i> , 2021, 17, e9536.	7.2	82
41	Proteomic cell surface phenotyping of differentiating acute myeloid leukemia cells. <i>Blood</i> , 2010, 116, e26-e34.	1.4	76
42	Quantitative analysis of human centrosome architecture by targeted proteomics and fluorescence imaging. <i>EMBO Journal</i> , 2016, 35, 2152-2166.	7.8	76
43	Immunity to Intracellular Salmonella Depends on Surface-associated Antigens. <i>PLoS Pathogens</i> , 2012, 8, e1002966.	4.7	74
44	Comparison of Different Sample Preparation Protocols Reveals Lysis Buffer-Specific Extraction Biases in Gram-Negative Bacteria and Human Cells. <i>Journal of Proteome Research</i> , 2015, 14, 4472-4485.	3.7	62
45	Differential scaling between G1 protein production and cell size dynamics promotes commitment to the cell division cycle in budding yeast. <i>Nature Cell Biology</i> , 2019, 21, 1382-1392.	10.3	61
46	Modularity and hormone sensitivity of the <i>Drosophila melanogaster</i> insulin receptor/target of rapamycin interaction proteome. <i>Molecular Systems Biology</i> , 2011, 7, 547.	7.2	60
47	Catechol siderophores repress the pyochelin pathway and activate the enterobactin pathway in <i>Pseudomonas aeruginosa</i> : an opportunity for siderophore-antibiotic conjugates development. <i>Environmental Microbiology</i> , 2016, 18, 819-832.	3.8	59
48	Quantitative Profiling of the Membrane Proteome in a Halophilic Archaeon. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1543-1558.	3.8	57
49	Protein Stoichiometry of a Multiprotein Complex, the Human Spliceosomal U1 Small Nuclear Ribonucleoprotein. <i>Journal of Biological Chemistry</i> , 2005, 280, 2536-2542.	3.4	52
50	High-accuracy proteome maps of human body fluids. <i>Genome Biology</i> , 2006, 7, 242.	9.6	50
51	Systems-Level Overview of Host Protein Phosphorylation During <i>Shigella flexneri</i> Infection Revealed by Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2952-2968.	3.8	50
52	Quantitative analysis of 2,3,7,8-tetrachlorodibenzo-p-dioxin-induced proteome alterations in 5L rat hepatoma cells using isotope-coded protein labels. <i>Proteomics</i> , 2006, 6, 2407-2421.	2.2	48
53	Quantitative isoform-profiling of highly diversified recognition molecules. <i>ELife</i> , 2015, 4, e07794.	6.0	48
54	Integrative proteogenomic characterization of hepatocellular carcinoma across etiologies and stages. <i>Nature Communications</i> , 2022, 13, 2436.	12.8	45

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55	Evaluation of Data-Dependent and -Independent Mass Spectrometric Workflows for Sensitive Quantification of Proteins and Phosphorylation Sites. <i>Journal of Proteome Research</i> , 2014, 13, 5973-5988.	3.7	44
56	Local Mitochondrial-Endolysosomal Microfusion Cleaves Voltage-Dependent Anion Channel 1 To Promote Survival in Hypoxia. <i>Molecular and Cellular Biology</i> , 2015, 35, 1491-1505.	2.3	40
57	SDHA gain-of-function engages inflammatory mitochondrial retrograde signaling via KEAP1-Nrf2. <i>Nature Immunology</i> , 2019, 20, 1311-1321.	14.5	39
58	Abundance of bacterial Type VI secretion system components measured by targeted proteomics. <i>Nature Communications</i> , 2019, 10, 2584.	12.8	35
59	Measuring glycolytic flux in single yeast cells with an orthogonal synthetic biosensor. <i>Molecular Systems Biology</i> , 2019, 15, e9071.	7.2	34
60	Benchmarking of analysis strategies for data-independent acquisition proteomics using a large-scale dataset comprising inter-patient heterogeneity. <i>Nature Communications</i> , 2022, 13, 2622.	12.8	34
61	Quorum sensing modulates the formation of virulent <i>Legionella</i> persisters within infected cells. <i>Nature Communications</i> , 2019, 10, 5216.	12.8	30
62	Comprehensive Description of the N-Glycoproteome of Mouse Pancreatic Î²-Cells and Human Islets. <i>Journal of Proteome Research</i> , 2012, 11, 1598-1608.	3.7	28
63	Extensive Mass Spectrometry-based Analysis of the Fission Yeast Proteome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1741-1751.	3.8	28
64	A bacterial type III secretion-based protein delivery tool for broad applications in cell biology. <i>Journal of Cell Biology</i> , 2015, 211, 913-931.	5.2	26
65	Stochastic Protein Alkylation by Antimalarial Peroxides. <i>ACS Infectious Diseases</i> , 2019, 5, 2067-2075.	3.8	23
66	Life-style changes of a halophilic archaeon analyzed by quantitative proteomics. <i>Proteomics</i> , 2009, 9, 3843-3855.	2.2	21
67	Proteomics of <i>Pyrococcus furiosus</i> ( <i>Pfu</i> ): Identification of Extracted Proteins by Three Independent Methods. <i>Journal of Proteome Research</i> , 2013, 12, 763-770.	3.7	21
68	Quorum sensing governs a transmissible <i>Legionella</i> subpopulation at the pathogen vacuole periphery. <i>EMBO Reports</i> , 2021, 22, e52972.	4.5	21
69	Mutations in respiratory complex I promote antibiotic persistence through alterations in intracellular acidity and protein synthesis. <i>Nature Communications</i> , 2022, 13, 546.	12.8	21
70	The SKP1-Cullin-F-box E3 ligase TrCP and CDK2 cooperate to control STIL abundance and centriole number. <i>Open Biology</i> , 2018, 8, .	3.6	20
71	Targeted proteoform mapping uncovers specific Neurexin-3 variants required for dendritic inhibition. <i>Neuron</i> , 2022, 110, 2094-2109.e10.	8.1	18
72	IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. <i>Journal of Proteomics</i> , 2011, 75, 116-121.	2.4	12

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73	Global Ion Suppression Limits the Potential of Mass Spectrometry Based Phosphoproteomics. <i>Journal of Proteome Research</i> , 2019, 18, 493-507.	3.7	12
74	Differential Plasma Glycoproteome of p19ARF Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. <i>Clinical Proteomics</i> , 2008, 4, 105-116.	2.1	11
75	RNA-bound PGC-1 $\beta$ controls gene expression in liquid-like nuclear condensates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	10
76	Evidence for a trap-and-flip mechanism in a proton-dependent lipid transporter. <i>Nature Communications</i> , 2022, 13, 1022.	12.8	10
77	Immunoaffinity Targeted Mass Spectrometry Analysis of Human Plasma Samples Reveals an Imbalance of Active and Inactive CXCL10 in Primary Sjögren's Syndrome Disease Patients. <i>Journal of Proteome Research</i> , 2020, 19, 4196-4209.	3.7	9
78	Quantitative Peptide and Protein Profiling by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 492, 21-38.	0.9	9
79	Cryo-EM structure of native human thyroglobulin. <i>Nature Communications</i> , 2022, 13, 61.	12.8	9
80	The timing of Start is determined primarily by increased synthesis of the Cln3 activator rather than dilution of the Whi5 inhibitor. <i>Molecular Biology of the Cell</i> , 2022, 33, rp2.	2.1	9
81	Measurement of <i>In Vivo</i> Protein Binding Affinities in a Signaling Network with Mass Spectrometry. <i>ACS Synthetic Biology</i> , 2017, 6, 1305-1314.	3.8	7
82	Mass spectrometry analysis of circulating breast cancer cells from a Xenograft mouse model. <i>STAR Protocols</i> , 2021, 2, 100480.	1.2	7
83	Exploiting the multiplexing capabilities of tandem mass tags for high-throughput estimation of cellular protein abundances by mass spectrometry. <i>Methods</i> , 2015, 85, 100-107.	3.8	5
84	Spatial proteomic and phospho-proteomic organization in three prototypical cell migration modes. <i>Proteome Science</i> , 2014, 12, 23.	1.7	4
85	Merged Map of the Yeast Proteome. <i>Cell Systems</i> , 2018, 6, 150-152.	6.2	3
86	Protocol for High-Yield Production of Photo-Leucine-Labeled Proteins in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2020, 19, 3100-3108.	3.7	3
87	Interactome and F-Actin Interaction Analysis of <i>Dictyostelium discoideum</i> Coronin A. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1469.	4.1	2
88	Defining Proteomic Signatures to Predict Multidrug Persistence in <i>Pseudomonas aeruginosa</i> . <i>Methods in Molecular Biology</i> , 2021, 2357, 161-175.	0.9	2